

#5

FIG. 1A

Sequence I

-72 AGGAAACCTGCC

-60 ATGGCCTCCTGGTGAGCTGTCTCATCCACTGCTGCTGCTCCTCTCCAGATACTCTGACCC

1 M D P L G A A K P Q W P W R R C L A A L

1 ATGGATCCCTGGGTGCAGCAAGCCACAATGGCCATGGCGCCGCTGTCTGGCCGCACTG

21 L F O L L V A V C F F S Y L R V S R D D

61 CTATTTACAGTGTGGTGGCTGTGTGTTTCTTCTCTACCTGCGTGTGTCCGAGACGAT

41 A T G S P R A P S G S S R Q D T T P T R

121 GCCACTGGATCCCCTAGGGCTCCCAGTGGTCTCCGACAGGACACCACTCCACCCGC

61 P T L L I L L W T W P F H I P V A L S R

181 CCCACCCTCTGATCCTGCTATGACATGGCCTTCCACATCCCTGTGGTCTGTCCCCG

81 C S E M V P G T A D C H I T A D R K V Y

241 TGTTACAGATGGTGCCCGCACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTAC

101 P Q A D T V I V H H W D I M S N P K S R

301 CCACAGGCAGACACGGTCACTCGTGACCACTGGGATATCATGTCCAACCTAAGTCACGC

121 L P P S P R P Q G Q R W I W F N L E P P

361 CTCCCACCTTCCCCGAGGCCGAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCC

141 P N C Q H L E A L D R Y F N L T M S Y R

421 CCTAACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTCTACCGC

161 S D S D I F T P Y G W L E P W S G Q P A

481 AGGACTCCGACATCTTCACGCCCTACGGCTGGTGGAGCCGTGGTCCGGCCAGCCTGCCA

181 H P P L N L S A K T E L V A W A V S N W

541 CACCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGGGGTGTCCCACTGG

FIG. 1B

201 K P D S A R V R Y Y Q S L Q A H L K V D
601 AAGCCGGA CTAGCCAGGTGCGTACTACTACAGAGCCTGCAGGCTCATCTCAAGGTGGAC

221 V Y G R S H K P L P K G T M M E T L S R
661 GTGTACGGACGCTCCACAAGCCCTGCCAAGGGACCATGATGAGACGCTGTCTCCCGG

241 Y K F Y L A F E N S L H P D Y I T E K L
721 TACAAGTTCTACCTGGCCTTCGAGAACTCCTTGACCCCGACTACATCACCGAGAAGCTG

261 W R N A L E A W A V P V V L G P S R S N
781 TGGAGGAACGCCCTGGAGGCTGGCGCTGCCCGTGGTGTGGTGGCCCCAGCAGAACCAAC

281 Y E R F L P P D A F I H V D D F Q S P K
841 TACGAGAGGTTCTCTGCCACCCGACGCCCTTCATCCAGTGGACGACTTCCAGAGCCCCAAG

301 D L A R Y L Q E L D K D H A R Y L S Y F
901 GACCTGGCCCGGTACTGCTGAGGAGCTGGACAAGACACGCCCGCTACCTGAGCTACTTT

321 R W R E T L R P R S F S W A L D F C K A
961 CGCTGGCGGAGACGCTGCGGCCCTCGCTCCTTCAGCTGGGCACTGGATTCTGCAAGGCC

341 C W K L Q Q E S R Y Q T V R S I A A W F
1021 TGCTGGAAACTGCAGCAGGAATCCAGGTACCAGACGGTGCGCAGCATAGCGGCTTGGTTC

361 T *
1081 ACCTGAGAGGCCGGCATGGTGCCCTGGGCTGCCGGGAACCTCATCTGCCTGGGGCCTCACC

1141 TGCTGGAGTCCTTTGTGGCCAACCTCTCTCTTACCTGGGACCTCACACGCTGGGCTTCA

1201 CGGCTGCCAGGAGCCTCTCCCCCTCCAGAAGACTTGCCCTGCTAGGGACCTCGCCTGCTGGG

1261 GACCTCGCCTGTTGGGACCTCACCTGCTGGGACCTCACCTGCTGGGACCTTGGCTGC

1321 TGGAGGCTGCACCTACTGAGGATGTGGCGGTCTGGGGACTTTACCTGCTGGGACCTGCTC
1381 CCAGAGACCTTGCCACACTGAATCTCACCTGCTGGGACCTCACCTGGAGGGCCCTGGG
1441 CCCTGGGGAACCTGGCTTACTTGGGGCCCCACCCGGGAGTGATGGTTCTGGCTGATTGTT
1501 TGTGATGTTAGCCGCTGTGAGGGGTGCAGAGAGATCATCACGGCACGGTTTCCAGA
1561 TGTAATACTGCAAGGAAAAATGATGACGTGTCTCCTCACTCTAGAGGGTTGGTCCCATG
1621 GGTTAAGAGCTCACCCAGGTTCTCACCTCAGGGGTTAAGAGCTCAGAGTTCAGACAGGT
1681 CCAAGTTCAAGCCAGGACCACCACTTATAGGGTACAGGTGGGATCGACTGTAAATGAGG
1741 ACTTCTGGAACATTCCAAATATTCTGGGGTTGAGGGAATTGCTGCTGTCTACAAAATGC
1801 CAAGGGTGACAGCGCTGTGGCTCAGCCCTGTAAATTCACGCACTTTGGGAGGCTGAGGT
1861 AGGAGGATTGATTGAGGCCAACAGTTAAAGACCAGCCTGGTCAATATAGCAAGACCACGT
1921 CTCTAAATAAAAAATAATAGCCGGCCAGGAAAAAATAAAAAA

FIG. 1C

FO402T" 54E9860

Sequence II

-276 CCTTCCCTTGTAGACTCTTCTTGGAATGAGAAGTAC
CGATTCTGCTGAAGACCTCGCGCTCTCAGGCTCTGGGAGTTGGAACCCCTGTACCTTCCTT
TCCTCTGCTGAGCCCTGCCTCCTTAGGCAGGCCAGAGCTCGACAGAACTCGGTTGCTTTG
CTGTTTGCTTTGGAGGGAACACAGCTGACGATGAGGCTGACTTTGAACCTCAAGAGATCTG
CTTACCCAGTCTCCTGGAATTAAGGCCCTGTACTACATTTGCCTGGACCTAAGATTTTC
1 M I T M L Q D L H V N K I S M S R S K S
1 ATGATCACTATGCTTCAAGATCTCCATGTCAACAAGATCTCCATGTCAAGATCCAAGTCA
21 E T S L P S S R S G S Q E K I M N V K G
61 GAAACAAGTCTTCCATCCTCAAGATCTGGATCACAGGAGAAAATAATGAATGTCAAGGGA
K V I L L M L I V S T V V V F W E Y V
41 AAAGTAATCCTGTTGATGCTGATTGTCTCAACCGTGGTTCGTGTTTGGGAATATGTC
121 N R I P E V G E N R W Q K D W W F P S W
61 AACAGAAATCCAGAGGTTGGTGAGAACAGATGGCAGAAAGGACTGGTGGTCCCAAGCTGG
181 F K N G T H S Y Q E D N V E G R R E K G
81 TTTAAATAATGGGACCCACAGTTATCAAGAAGACAAACGTAGAAGGACGGAGAGAAAAGGCT
241 R N G D R I E E P Q L W D W F N P K N R
101 AGAAATGGAGATCGCATTTGAAGAGCCTCAGCTATGGGACTGGTTCAATCCAAAGAACCCGC
301 P D V L T V T P W K A P I V W E G T Y D
121 CCGGATGTTTGTGACAGTGACCCCGTGGAGGCCCGCATTTGTGTGGGAAGGCCACTTATGAC
361

FIG. 2A

FIG. 2B

141	T A L L E K Y Y A T Q K L T V G L T V F
421	ACAGCTCTGCTGGAAGTACTACGCCACACAGAACTCACTGTGGGCTGACAGTGTTT
161	A V G K Y I E H Y L E D F L E S A D M U
481	GCTGTGGAAAGTACATTGAGCATTACTTAGAAGACTTTCTGGAGTCTGCTGACATGTAC
181	F M V G H R V I F Y V M I D D T S R M P
541	TTCATGGTTGGCCATCGGTCATATTTTACGTCATGATAGACGACACCTCCCGGATGCCT
201	V V H L N P L H S L Q V F E I R S E K R
601	GTCGTGCACCTGAACCTCTACATTCCTTACAAGTCTTTTGAGATCAGTCTGAGAAGAGG
221	W Q D I S M M R M K T I G E H I L A H I
661	TGGCAGGATATCAGCATGATGGCATGAAGACCATTGGGGAGCACATCCTGGCCACATC
241	Q H E V D F L F C M D V D Q V F Q D N F
721	CAGCAGAGGTCGACTTCCTCTCTGTCATGGACGTGGATCAAGTCTTTCAAGACAACCTC
261	G V E T L G Q L V A Q L Q A W W Y K A S
781	GGGTGGAAACTCTGGCCAGCTGGTAGCACAGCTCCAGGCCCTGGTGTACAAGGCCAGT
281	P E K F T Y E R R E L S A A Y I P F G E
841	CCCGAGAAGTTCACCTATGAGAGCGGGAACCTGTGGCCGCGTACATTCCTTCGGAGAG
301	G D F Y Y H A A I F G G T P T H I L N L
901	GGGGAATTTTACTACACGCGGCCATTTTGGAGGAACGCTACTCACATTTCTCAACCTC
321	T R E C F K G I L Q D K K H D I E A Q W
961	ACCAGGAGTGCTTTAAGGGGATCCTCCAGGACAAGAAACATGACATAGAAGCCAGTGG
341	H D E S H L N K Y F L F N K P T K I L S
1021	CATGATGAGAGCCACCTCAACAAATACTTCCTTTTCAACAACCCACTAAAATCCTATCT

FIG. 2C

361 P E Y C W D Y Q I G L P S D I K S V K V
1081 CCAGAGTATTGCTGGGACTATCAGATAGGCCTGCCCTTCAGATATTAAAGTGTC AAGGTA
381 A W Q T K E Y N L V R N N V *
1141 GCTTGGCAGACAAAAGAGTATAATTGGTTAGAAATAATGTC T GACTTCAAATTGTGATG
1201 GAAACTTGACACTATTCTAACCA

FIG. 2C

Sequence III

10	20	30	40	50	60
GAATTCCATCGTGGCAAGGCAGCCCTGAATGGATGATGTAACCTGGGGTCTTCAATGG					
70	80	90	100	110	120
AGGGCCAGACTCCTGGGTCTAGGGGATGAGGGGAGGGAGGATCGGGTTAGCTGGGACCCA					
130	140	150	160	170	180
GGTGAAGGGGCTGGGGGCCACATTCCTGAGTCTCAGAGAGAAGGATCTGGGGTCTCAA					
190	200	210	220	230	240
GCACCTGAGTCGGAGGGAGGGGTGCTGGGCTCCTGGAAAAAACCACTCTTGGACCAT					
250	260	270	280	290	300
CTATGCAGATCAGCAGAACAAAGAGAAATTTCTGGCCCCCATCTGAATTTCTAAGTTGG					
310	320	330	340	350	360
GGGAGGGCGTGATCTGACACTGAGGTTCTTGATCCTCAGCAAGCGGCAATTGCTGTA					
370	380	390	400	410	420
TGAAAGAAGCAGCCGCATCTGAGACACAAGTATCCTGCCTTGGAGCCTCTCACCTGGCC					
430	440	450	460	470	480
GTGGGCCAACCTCAACCTCATCTGTCCCTGCTCAGATGCTCAGACCCCTGGACATCCCAGC					
490	500	510	520	530	540
CTCCTCCTCCTGATGCAATCCTGGTGTCTTTTCCACAGAGAAGCCATCCCAGGCCAG					
550	560	570	580	590	600
GCAGGTGCTCCTGAAATAACCTGGGGGAGGGGTGGCTGAAAGTCCCTGACTGGAGTTGG					
610	620	630	640	650	660
CAGCCAAGCCAGGCCCTGGAGTGGGGCACCCAGAGGGAAGACAGGTTGGCTAATTTCTCTGG					

FIG. 3A

FIG. 3B

FIG. 3B

670 680 690 700 710 720
AGCCCCAAGGGTGCAAGGCTAGGCCCTTCTGTCTGAGGGAGGAGGCTGGGCTCTGG
730 740 750 760 770 780
ACTCCTGGGTCTGAGGGAGGAGGGGTGGGGCCCTGGACTCCTGGGTCTGAGGGAGGAGG
790 800 810 820 830 840
GTCTGGCCCTGTACTCCTGGATCTGAGGGAGGGGCTGGGGAACCTTGGGCTCCTGGGT
850 860 870 880 890 900
CTGAGGGAGGAGGAGCTTTGGTCTGGACTCCTGGGTCTGAGGGAGTAGGGCTAGGGAT
910 920 930 940 950 960
CTGGAATCGTGGGTGTGAGGAAGGAGGGGCTGGGTCTGGACTCCTGGGTCTGAGGAAG
970 980 990 1000 1010 1020
GAGGGCAGGGGCTTGGACTCCTGGGTCTGAGGAAGGAGGGCCGGAGCCTGGACTCC
1030 1040 1050 1060 1070 1080
TAAGTCTGAGGGAGGGTCTGGGGCCCTGGACTGCTGGGTGTGAGCACAAAGGTCTGG
1090 1100 1110 1120 1130 1140
GTGCTGGGAGTCCCGAGCCCTGGGAGATGATGGTTAAACTTCTGGGAATCAAGTCAAAC
1150 1160 1170 1180 1190 1200
CCTGAGTCTTTGACATTGATGTATCTTGAATGGGAGGTCAGTCTGTGGGAAGGATTAC
1210 1220 1230 1240 1250 1260
CCAGGTGCCGAGGCAAGAGACTGAAGGCACAACTGTTTCAGTATAATAAGAAAATAGT
1270 1280 1290 1300 1310 1320
TAGAATAAGAAATAGTTATCATACAAATTAGATATAGAGATGATCATGGACAGTATCAATC

1330 1340 1350 1360 1370 1380
ATTAGTGAAACATTATTAATCATTAGCTATTACTTTTATTCTTTGTTGATAACTAATA
1390 1400 1410 1420 1430 1440
TAACCAGGAACAACCGGTGGGTATAGGGTCAGGTACTGAAGGGACATTGTGAGAGTGA
1450 1460 1470 1480 1490 1500
CCTAGAAGCAAGAGGTGAGCCTTCTGTCAACCCGGCATAAGGGCCTCTTGAGGGCTCCT
1510 1520 1530 1540 1550 1560
TGGTCAAGGGGAACGCCAGTGTCTGGGAAGGACCCGTTACTCAGCAGACCACGAAAGG
1570 1580 1590 1600 1610 1620
GAATCTCCTTTTCTTGGAGGAGTCAGGGAACACTCTGCTCCACCAGCTTCTTGTGGGAGG
1630 1640 1650 1660 1670 1680
CTGGGTATTATCTAGGCCCTGCCCGCAGTCATCCTGCTGTGTGCTTCAATGGTCACGC
1690 1700 1710 1720 1730 1740
TCCTTGTCCTCTTGCAATTTTCTCCCGTACTCCTGGTCTCTTTGAAGTTCGTAGTAGA
1750 1760 1770 1780 1790 1800
TAGCGGTAGAGAAATAGTGAAAGCCTTTTCTTTTGTGAGCGGAGTCTCGCTC
1810 1820 1830 1840 1850 1860
TGTCGCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAATCTCCGCCCTCCTGG
1870 1880 1890 1900 1910 1920
GTTACACCAATTCTCCTGCCCTCACCCCTCCCAAATAGCTAGGACTACAGGCGCCCTCCACC
1930 1940 1950 1960 1970 1980
ACGCGCCCGGATAATTTTGTGATTTTATAGTAGACAGGGTTTCAACCGTGTAGCCAGG

FIG. 3C

FIG. 3D

1990 2000 2010 2020 2030 2040
ATGGCCTCACCTCCTGACCTTGTGATCCGCCCGCCTCAGCCTCCCAAAGTGCTGGGATT

2050 2060 2070 2080 2090 2100
ACAGCGTGAGCCACCGCGCCCGCGAAATAGTGAAGTCTTAAAGTCTTTGATCTTTC

2110 2120 2130 2140 2150 2160
TTATAAGTGCAGAGAAGAAAACGCTGACATATGCTGCCTTCTCTTCTGCTTCGGCTGCC

2170 2180 2190 2200 2210 2220
TAAAGGGAAGGGCCCCCTGTCCCATGATACGTGACTTGCTTGACCTTATCAGTCATTT

2230 2240 2250 2260 2270 2280
GGACGACTCACCCCTCCTTATCCTGCCCCCCTTGCTTGTATACAATAAATATCAGCGCG

2290 2300 2310 2320 2330 2340
CCAGCCATTGCGGGCCACTACCGGCTCTCTGGCTCTTGATGGTAGTGTCCTCCCGGGCCC

2350 2360 2370 2380 2390 2400
AGCTGTTTCTCTTTATCTCTTTGTCTTGTGCTTTTATTCTTACAAATCTCTCTCTCCT

2410 2420 2430 2440 2450 2460
CACAGGGAAGAACACCCACCCGCAAGCCCCGTAGGGCTGGACCTACGTTAGCCTGCC

2470 2480 2490 2500 2510 2520
CTGCTCGGGTTGGCGATGCTGGAGTGGGCTTGAGACCAGAGAAAATGCTTAAATTAGG

2530 2540 2550 2560 2570 2580
TGACAAAGCGGCAGAGGCCCTTGTCTCTGGCGCCGCGACGCCCGCCCGCTGACGGCG

2590 2600 2610 2620 2630 2640
TGGGAAACAGACCCCTGTTCCACTCCGGTCTCCAGCCTTGGAATGGTTGCCCTCGTGCAGT

2650 2660 2670 2680 2690 2700
 GCAGGTCTGGAAAGTAGCAGTTTGGACGGGACCCTAGAAATCCCCAAAGAGTACTA
 2710 2720 2730 2740 2750 2760
 GGGGCTGGGATTCTGGAATTGAGTGTGGACGGTAGGCGGGGGGTGTGGAGATCGGAG
 2770 2780 2790 2800 2810 2820
 ACCCTGGTGGGCGGGAGCACCTGCAGGCTGGAGGCCCTCGCGCGTCCGGCGGCAGCC
 2830 2840 2850 2860 2870 2880
 TGGCAACACAGGTTCTCCATCCCCCAGGAGGACGCGGCAGAGGGGACGATCGTCCACT
 2890 2900 2910 2920 2930 2940
 CGCCGGGACCAAGGTGCGGGGCCCTGCCAGCCGCTGGGGCGTGGCCAGGCTCGAAGCAC
 2950 2960 2970 2980 2990 3000
 CCAGGTGTCGGGGGCCGACTCTAAGCCCTGGCACCGGAAGAGAGAGGGCGCGGATTGGA
 3010 3020 3030 3040 3050 3060
 CCTCCCGGCTCCAGCATTGCAACTGGGCGCTCCGTCTCTGTGTCCACGCAATGATGCTGC
 3070 3080 3090 3100 3110 3120
 GGCTGCTCAGAAGCCAGGTAGCCTGCCCTGGGTGAAGCCTTCGCGCAGGTCAATGACGGG
 3130 3140 3150 3160 3170 3180
 GCGGAGGGGCAGGGCGGGTCCCCCTGCATCCCCGATCTGGGAGCGGTGGGCCACAGGGC
 3190 3200 3210 3220 3230 3240
 CATCGCCTTAGCCCCCTGGCGCTGGGGCTCGGCGCCAAAGTACGGGCGGGGCTCCACCTTC
 3250 3260 3270 3280 3290 3300
 CAGCCATCCGCCCGGCCGGAGGGGACGCTGCGAGACTCCCGGCGCGGCCCTCTCCT

FIG. 3E

FIG. 3F

3310 3320 3330 3340 3350 3360
TCCTCTCCTCCCAAGCCCTCGCTGCCAGTCCGGACAGGCTGCGGAGGGAGGGCTGC

3370 3380 3390 3400 3410 3420
CGGGCCGGATAGCCGGACGCCCTGGCGTTCAGGGCGGCGGATGTGGCCTTGCTTGGC

3430 3440 3450 3460 3470 3480
GAGGGTCCGCTCCGGCCACGAAAGCGGACTGTGGATCTGCCACCTGCAAGCAGCTCGGC

3490 3500 3510 3520 3530 3540
TAAGTGGGACTGCCCCACTCAGTTGTTCTCTGGGACCCAGGAACAACCTCTCAGAACCA

3550 3560 3570 3580 3590 3600
GGAGGTGACCCCAACCTCTTCTCCAGGTCTTCTAAGGCCCTAGGAATCTCCGCCACC

3610 3620 3630 3640 3650 3660
TCCCCAGCCATTACTCCTCCAGGAACCAAGATGCTCTTCCGCTCCTGACCCCTCCAGCCT

3670 3680 3690 3700 3710 3720
CTCTTGTTTACTTGAACTATCGTTTCCCATCACCACTCTGTGGTGGATTTTGGCCCTC

3730 3740 3750 3760 3770 3780
ACAGACAGGTACTCCTGAGAAACAGGCTGGTGGAGAGTCCAGTATCAGCGGAACCTTASC

3790 3800 3810 3820 3830 3840
AGGAGGGGAGACTCGAGATTCTTTCAGGAAAGGTGTAGGAACCTGGACCACTTCTTTT

3850 3860 3870 3880 3890 3900
TTTTTTTTTTTTTTTAAAGACAGGTCCTCTCTGTGCGCGCAAGCTGGAGTGCAGTCAG

3910 3920 3930 3940 3950 3960
CGGTGCTATCGGGGCTCATTTGTGAGCTCCGGGGATCCTCCCGCCTTAGCATCCGGGTAG

TOTAL 9248860

FIG. 36

3970 3980 3990 4000 4010 4020
 CTGAGACCACAGACATGTGCCACCATGCCAAGCTAATTTTATTATTTTGTGGAGAC
 4030 4040 4050 4060 4070 4080
 GGAGTTTCACTCTTGTGCCCAGGCTGGAGTGTAATGGCATGATCTCAGCTCACCGCAAC
 4090 4100 4110 4120 4130 4140
 TCCCCCCCCGGGTTTCAGGCGATTCTCCTGCCCTCAGCCTCCCGAGTGGCTGGGATTACA
 4150 4160 4170 4180 4190 4200
 GGCAITCGCCACCATGCCCCGGCTAATTTTGATTTTAAGTAGACAGGGTTTCTCCACG
 4210 4220 4230 4240 4250 4260
 TTGGTCAGGCTGGTCTCGAACTCCCAACCTCAGGTGATCCACCCACCTTGGCCTCCCAA
 4270 4280 4290 4300 4310 4320
 GTGCTGGGATTACAGGTGTGAGCCACCGCGCTGGCCCATGCCAAGCTAATTTTAAAT
 4330 4340 4350 4360 4370 4380
 TTTTGTAGAGTGCTCTGTGTTGCCAGGCTGATCTTGAACCTCTGGGCTCAAGGGATCCT
 4390 4400 4410 4420 4430 4440
 CCCATCTCAGCCTCCCAATATGTCTGGGATTACAGGTGTGAGCCACAGTGCCAGCCAAAC
 4450 4460 4470 4480 4490 4500
 CATGGCTATCTTGAAACCACTTGCTTCCAGTCCCAATGCCCGAAATTCGAAGGCTCT
 4510 4520 4530 4540 4550 4560
 CATCCCTGAAACCTAGGACTCAGGCTCTCCCTACCTCAGCCCCCAGGAGTCTAAACCTTA
 4570 4580 4590 4600 4610 4620
 ACTTCCCTCTTCCCTGGGACTAAGGAGTGCTGCACCCAGGCGCTCCCTTACCCACAT

4630 4640 4650 4660 4670 4680
CCCTCCTCAGCCTCCCTCCTCAGCCTCAGTGCAATTGCTAATTGCGCTTTTCTCCTCCCTG
4690 4700 4710 4720 4730 4740
CAGCCATGTGGCTCCGGAGCCATCGTCAGCTCTGCCTGGCCTTCTCTGCTAGTCTGTGTCC
MetTrpLeuArgSerHisArgGlnLeuCysLeuAlaPheLeuValCysValL
4750 4760 4770 4780 4790 4800
TCTCTGTAATCTTCTCCTCATATCCATCAAGACAGCTTCCACATGGCCTAGGCCTGT
euSerValIlePhePheLeuHisIleHisGlnAspSerPheProHisGlyLeuGlyLeuS
4810 4820 4830 4840 4850 4860
CGATCCTGTGTCCAGACCGCCGCTGGTGACACCCCGAGTGGCCTTCTGCTGCTGCGG
erIleLeuCysProAspArgArgLeuValThrProProValAlaIlePheCysLeuProG
4870 4880 4890 4900 4910 4920
GTACTGCGATGGGCCCCAACGCCCTCCTCTCTGTCCTCCAGCACCTGCTTCTCCTCTCCG
lyThrAlaMetGlyProAsnAlaSerSerCysProGlnHisProAlaSerLeuSerG
4930 4940 4950 4960 4970 4980
GCACCTGGACTGTCTACCCCAATGGCCGGTTTGGTAATCAGATGGGACAGTATGCCACGC
lyThrTrpThrValTyrProAsnGlyArgPheGlyAsnGlnMetGlyGlnTyrAlaThrL
4990 5000 5010 5020 5030 5040
TGCTGGCTCTGGCCAGCTCAACGGCCCGCCGCTTATCTGCTGCTGCCATGCATGCCG
euLeuAlaLeuAlaGlnLeuAsnGlyArgArgAlaPheIleLeuProAlaMetHisAlaA
5050 5060 5070 5080 5090 5100
CCCTGGCCCCGGTATTCCGCATCACCTGCCCGTGTGGCCCCAGAAAGTGGACAGCCGCA
laLeuAlaProValPheArgIleThrLeuProValLeuAlaProGluValAspSerArgT
5110 5120 5130 5140 5150 5160
CGCCGTGGCGGAGCTGCAGCTTCACGACTGGATGTGGAGGAGTACGGGACTTGAGAG
hrProTrpArgGluLeuGlnLeuHisAspTrpMetSerGluGluTyrAlaAspLeuArgA

FIG. 3H

5170 5180 5190 5200 5210 5220
 ATCCTTCTGAAGCTCTCTGGCTTCCCTGCTCTTGGACTTCTTCCACCATCTCCGGG
 spPropheLeuLysLeuSerGlyPheProCysSerTrpThrPhePheHisHisLeuArgG
 5230 5240 5250 5260 5270 5280
 AACAGATCCGACAGAGATTACCCCTGCACGACACCTTCGGGAAGAGCGCAGAGTGTGC
 luGlnIleArgArgGluPheThrLeuHisAspHisLeuArgGluGluAlaGlnSerValL
 5290 5300 5310 5320 5330 5340
 TGGGTCAGCTCCGCTGGCCGCACAGGGACCGCCCGCACCTTGTGGCGTCCACG
 euGlyGlnLeuArgLeuGlyArgThrGlyAspArgProArgThrPheValGlyValHisV
 5350 5360 5370 5380 5390 5400
 TCGCCGTGGGGACTATCTGCAGGTTATGCCTCAGCGCTGGAAGGTGTGGTGGCGACA
 alArgArgGlyAspTyrLeuGlnValMetProGlnArgTrpLysGlyValValGlyAsps
 5410 5420 5430 5440 5450 5460
 GCGCCTACTCCGGCAGGCCATGGACTGGTTCCGGGCACGGCACGAAGCCCCGTTTCG
 erAlaTyrLeuArgGlnAlaMetAspTrpPheArgAlaArgHisGluAlaProValPheV
 5470 5480 5490 5500 5510 5520
 TGGTCACCAAGCAACGGCATGGAGTGGTGTAAAGAAACATCGACACCTCCAGGGCGATG
 alValThrSerAsnGlyMetGluTrpCysLysGluAsnIleAspThrSerGlnGlyAspV
 5530 5540 5550 5560 5570 5580
 TGACGTTTGTGGCGATGGACAGGAGGCTACACCGTGGAAAGACTTTGCCCTGCTCACAC
 alThrPheAlaGlyAspGlyGlnGluAlaThrProTrpLysAspPheAlaLeuLeuThrG

FIG. 3I

5590 5600 5610 5620 5630 5640
AGTGAACACACACATTATGACCATTGGCACCTTCGGCTTCTGGCTGCCTACCTGGCTG
InCysAsnHisThrIleMetThrIleGlyThrPheGlyPheTrpAlaAlaTyrLeuAlaG
5650 5660 5670 5680 5690 5700
GCGGAGACACTGTCTACCTGGCCAACTTCACCCCTGCCAGACTCTGAGTTCTCTGAAGATCT
lyGlyAspThrValTyrLeuAlaAsnPheThrLeuProAspSerGluPheLeuLysIleP
5710 5720 5730 5740 5750 5760
TTAAGCCGGAGCGGCCTTCCTGCCCGAGTGGTGGGCATTAAATGCAGACTTGTCTCCAC
heLysProGluAlaAlaPheLeuProGluTrpValGlyLeuAsnAlaAspLeuSerProL
5770 5780 5790 5800 5810 5820
TCTGGACATTGGCTAAGCCTTGAGAGCCAGGGAGACTTCTGAAAGTAGCCTGATCTTTCT
euTrpThrLeuAlaLysProEnd
5830 5840 5850 5860 5870 5880
AGAGCCAGCAGTACGTGGCTTCAGAGGCCCTGGCATCTTCTGGAGAAGCTTGTGGTGTTC
5890 5900 5910 5920 5930 5940
TGAAGCAAATGGGTGCCCGTATCCAGAGTGATTCTAGTTGGGAGAGTTGGAGAGAAGGGG
5950 5960 5970 5980 5990 6000
GACGTTTCTGGAACTGTCTGAATATTCTAGAACTAGCAAAACATCTTTCTGATGGCTG
6010 6020 6030 6040 6050 6060
GCAGGCAGTTCTAGAAAGCCACAGTGCCCACTGCTCTTCCCAGCCCCATATCTACAGTACT
6070 6080 6090 6100 6110 6120
TCCAGATGGCTGCCCCCAGGAATGGGAACTCTCCCTCTGTGTCTACTCTAGAAGAGGGGT
6130 6140 6150 6160 6170 6180
TACTTCTCCCCCTGGGTCTCCAAAGACTGAAGGAGCATATGATTGCTCCAGAGCAAGCAT

FIG. 3J

6190 6200 6210 6220 6230 6240
TCACCAAGTCCCCCTTCTGTGTTTCTGGAGTGATTCTAGAGGGAGACTTGTCTTAGAGAGG

6250 6260 6270 6280 6290 6300
ACCAGGTTTGATGCCCTGTGAAGAACCCTGCAGGGCCCTTATGGACAGGATGGGTTCTTGG

6310 6320 6330 6340 6350 6360
AAATCCAGATAACTAAGGTGAAGAACTTTTTTAGTTTTTTTTTTTTTTTTTTGGAGACAG

6370 6380 6390 6400 6410 6420
GGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGTGATCTTGGCTCACTGCAACTTC

6430 6440 6450 6460 6470 6480
CGCCTCCTGTGTTCAAGCGATTCTCCTGTCTCAGCCCTCCTAGTAGATGGGACTACAGGC

6490 6500 6510 6520 6530 6540
ACAGGCCATTATGCCCTGGCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACCATGTT

6550 6560 6570 6580 6590 6600
GGCCGGGATGGTCTCGATCTCCTGACCTTGTCATCCACCTGTCTTGGCCTCCCAAAGTGC

6610 6620 6630 6640 6650 6660
TGGGATTACTGGCATGAGCCACTGTGCCCCAGCCCCGGATATTTTTTTTAAATTATTTATT

6670 6680 6690 6700 6710 6720
ATTTATTTATTATTGAGACGGAGTCTTGCTCTGTAGCCCCAGGCCAGAGTGCAGTGGCGC

6730 6740 6750 6760 6770 6780
GATCTCAGCTCACTGCAAGCTCTGCCCTCCCGGGTTTCATGCCATTCTGCTCAGCCTCCTG

6790 6800 6810 6820 6830 6840
AGTAGCTGGGACTACAGGGCGCCCCCACCACGCCCGGCTAATTTTTTTTGTATTTTAGT

FIG. 3K

FIG. 3L

6850	6860	6870	6880	6890	6900
AGAGACGGGTTTCATCGTTTAA	CCAGGATGGTCTCGATCTCCTG	ACCTCGTGATCTGC			
6910	6920	6930	6940	6950	6960
CCACCTCGGCCCTCCACAGTGTG	GGATTACCGCGGTGAGCCACCATG	CCTGGCCCGGAT			
6970	6980	6990	7000	7010	7020
AAATTTTAAATTTTGTAGAGACG	AGGTCTTGTGATATTGCCCAGGCTG	TTCTTCAAC			
7030	7040	7050	7060	7070	7080
TCCTGGGCTCAAGCAGTCTCTCC	ACCTTGGCCTCCAGAAATGCTGG	TTTATAGATGTGA			
7090	7100	7110	7120	7130	7140
GCCAGCACACCGGGCCAAAGTGA	AGAACTAATGTGCAACCTAATTG	TAGCATCTAA			
7150	7160	7170	7180	7190	7200
TGAATGTTCCACCATTTGCTGG	AAAAATTGAGATGGAAAAACAAC	CATCTCTAGTTGGCCA			
7210	7220	7230	7240	7250	7260
GCGTCTTGCTCTGTTCACAGTCT	CTGAAAAAGCTGGGGTAGTTGG	TGAGCAGCGGGAC			
7270	7280	7290	7300	7310	7320
TCTGTCCAAACAAGCCCCACAG	CCCCCTCAAAGACTTTTTTTT	TGTTTGAGCAGACAG			
7330	7340	7350	7360	7370	7380
GCTAAATGTGAACGTGGGGTG	AGGGATCACTGCCAAAAATGGT	ACAGCTTCTGGAGCAGA			
7390	7400	7410	7420	7430	7440
ACTTTCCAGGGATCCAGGGACA	CTTTTTTTTAAAGCTCATAA	ACTGCAAGAGCTCCATA			
7450	7460	7470	7480	7490	7500
TATTGGGTGTGAGTTCAGGTG	CCCTCTCACAAATGAAGGA	AGTTGGTCTTTGTCTGCAGGT			

7510	7520	7530	7540	7550	7560
GGGCTGCTGAGGGTCTGGGATCTGTCTTTTCTGGAAGTGTCAGGTATAAACACACACCCTCTG					
7570	7580	7590	7600	7610	7620
TGCTTGTGACAAACTGCAGTAACCGTGCTCATTTGCTAACCACCTGTCTGTCCCTGAACCTC					
7630	7640	7650	7660	7670	7680
CCAGAACCACCTACATCTGGCTTTGGGCAGGTCTGAGATAAAACGATCTAAAGGTAGGCAG					
7690	7700	7710	7720	7730	7740
AACCTGGACCCAGCCTCAGATCCAGGCAGGAGCACGAGGTCTGGCCAAGGTGGACGGGT					
7750	7760	7770	7780	7790	7800
TGTCGAGATCTCAGGAGCCCCCTTGCTGTCTTTTGGAGGGTGAAAGAAGAAACCTTAAACA					
7810	7820	7830	7840	7850	7860
TAGTCAGCTCTGATCACATCCCCTGTCTACTCACTCCAGACCCCATGCCCTGTAGGCTTATC					
7870	7880	7890	7900	7910	7920
AGGGAGTTACAGTTACAATTGTTACAGTACTGTTCCTCCAACTCAGCTGCCACGGGTGAGAG					
7930	7940	7950	7960	7970	7980
AGCAGGAGGTATGAATTAAAAGTCTACAGCACTAACCCGTGTCTCTGTAGCTTTTTTTGGA					
7990	8000	8010	8020	8030	8040
GCCAGAGCCACTGTGTA GTGTGTGTGGGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT					
8050	8060	8070	8080	8090	8100
AAAGAGAGTGGAGGAAAAAGGTGGGGTACTTCTGAAGACTTTTATTTTTTTTAAATTAATTT					
8110	8120	8130	8140	8150	8160
ATTTTTTTCAGAGATCGAGTCTTGCTCTGTGGCCCGGCTGGAGTGCAGTAGTGTGATC					

FIG. 3M

FIG. 3N

8170
TCGGCCCACTGCAA

FIG. 3N

10	20	30	40	50	60
* GAGAG CGCCA CCCGG AAGCC ACTTT TATAG AAGCT TTTAC ACACA ATGCT TGATT					
70	80	90	100	110	120
* TTTT TTTT TTTT CGAGA CGGAG TCTCG CTTTG TCGCC CAGGC TGGAG TGCAG TGGCG					
130	140	150	160	170	180
* TGGC TCACT GCAAG CTCCG CCTCC TGGGT TGACG CCATT CTCCT GCCTC AGCTT					
190	200	210	220	230	240
* GTAGC TGGGA CTACA GCGC CCGC ACCAA GCCTG GCTAA TTTT TTTT					
250	260	270	280	290	300
* AGACA GAGTT TCACC GTGTT AGCCA GGATG GTCCTC GATCT CCTGA CCTCG GGATC					
310	320	330	340	350	360
* GCCTC GGCCT CCCAA AGTGC TGGGA GTATA GGCGT GAGCC ACCGC GCCTG GCCTA					
370	380	390	400	410	420
* GATT TTAAT GAAAA CATT TTAAT ATGGC TAACG CAAAT TTATT TTCTG					
430	440	450	460	470	480
* ATAAC ATCAA AAACA CCTGG CAGGA CTGCC CCATT CCCAG CACTG TCTAG TTCTC					

FIG. 4A

FIG. 4B

490	500	510	520	530	540
* CCCTA GTATC AGTGG GACTC CACTG ATGCA CAGCT GTGAT CTACT AAAAC TTCTC TCAAA	* 560	* 570	* 580	* 590	* 600
* ACTTT CTCCT CTCCT TAGGT CAGCA GCCCC TGATC TATTT GGAAA TCCCC TGAAT	* 620	* 630	* 640	* 650	* 660
* AAAAA TTGAA TATCA TAAAC CAAAG CGAAC ACCCA GAAAT TCAAA TTCAA CCCGT AGGTA	* 680	* 690	* 700	* 710	* 720
* AAAAA TTTCT CAAGT GACTG TAGAC GTAGA TGTTCT CCAGT GTCGC CTAAT AAGGT AGAAG	* 740	* 750	* 760	* 770	* 780
* AGGCC AGTGC GATAC TGTCT TTACA CCCTT AACTT GGGTG CTAGA ATATT TATCT TCGTC	* 800	* 810	* 820	* 830	* 840
* ATCAT TTTAT CATCC AAACT ATTTT GCATA ACTTT CATGG GTGCA GAAAA TGTTT TTTAA	* 860	* 870	* 880	* 890	* 900
* GTGCT TGGTA AAATT AATAG TGATA TTCAT TCATT CATCT CACTG AACAG GCAAT AAATT					
* 910	* 920	* 930	* 940	* 950	* 960
* CCTTG ACGAC AAGGG CCTTG GGGGG GGCCA CATCT TCATC TTTGG TTTAT GAGTC CTGTG					

FIG. 4B

970	980	990	1000	1010	1020
* CGTCT TGGTA CAAGC AATAC TACTA TGAGC CGGCA AGTCA GACTT ATTTG GTAGG GGACC	* 1040	* 1050	* 1060	* 1070	* 1080
1030	1040	1050	1060	1070	1080
* AAAGG AAAGA ACATG TTTTG ATTGC TAAGA AAACA TTTTG TTCTC TATTC TTTAC TGGGC	* 1100	* 1110	* 1120	* 1130	* 1140
1090	1100	1110	1120	1130	1140
* TGGCA GGCAA AGGAA ATGTT CTTAT GAGCA CTCAC ATTGA AAAC TAAAGT TCTTC ACCAA	* 1160	* 1170	* 1180	* 1190	* 1200
1150	1160	1170	1180	1190	1200
* ATGCA GAGAC TCTGA AGGCC ACGCC GCTGC GGGCT GCCTC CACAA TTCGA CCGTC TCGGC	* 1220	* 1230	* 1240	* 1250	* 1260
1210	1220	1230	1240	1250	1260
* GGGCC ACGAG ATCCT GGCCA CGGAT GCGGT GGCCG CGCCT CTGCT CGCAC GTTCC CCCGG	* 1280	* 1290	* 1300	* 1310	* 1320
1270	1280	1290	1300	1310	1320
* CCTCT GGA CTCTC CCTCC CTCAA TCCCT CCCTC CGGCG GGCGT CGCTG GCGGG TGGCT	* 1340	* 1350	* 1360	* 1370	* 1380
1330	1340	1350	1360	1370	1380
* AGGCC CAACG GCAGG AAGCC GACGC TATCC TCCGT TCCGC GCGCG CCGGT CCGCC TTCCG	* 1400	* 1410	* 1420	* 1430	* 1440
1390	1400	1410	1420	1430	1440
* TCTGT TCTAG GGCCT GCTCC TCGCG GGCAG CTGCT TTAGA AGGTC TCGAG CCTCC TGTAC					

FIG. 4C

FIG. 4D

1450	1460	1470	1480	1490	1500
* CTTCC CAGGG ATGAA CCGGG CCTTC CCTCT * GGAAG GCGAG GGTTT GGGCC ACAGT GAGCG					
1510	1520	1530	1540	1550	1560
* AGGGC CAGGG CCGTG GCGGC GCGCA GAGGG AAACC GGATC AGTTG AGAGA GAATC AAGAG					
1570	1580	1590	1600	1610	1620
* TAGCG GATGA GCGGC TTGTG GGGCG CCGCC CGGAA GCCCT CCGGC CCGCT GGGG AGAAG					
1630	1640	1650	1660	1670	1680
* GAGTG GCGCG AGGCG CCGCA GGAGG CTCCC CCGGC CTGGT CCGGC CCGCT GGGCC CCGGG					
1690	1700	1710	1720	1730	1740
* CGCAG TGGAA GAAAG GGACG GCGCG TGCCC GGTG GCGT CCTGG CCAGC TCACC TTGCC					
1750	1760	1770	1780	1790	1800
* CTGGC GGCTC GCCCG GCCCG GCACT TGGGA GGAGC AGGGC CCGCG GCCTT TGCAT					
1810	1820	1830	1840	1850	1860
* TCTGG GACCG CCCCC TTCCA TTCCC GGGCC AGCGG CGAGC GGCAG GCTGG AGCCG					
1870	1880	1890	1900	1910	1920
* CAGCT ACAGC ATGAG AGCCG GTGCC GCTCC TCCAC GCCTG CCGAC GCGTG GCGAG CGGAG					

FIG. 4D

DOCKET #2449860

1930 * 1940 * 1950 * 1960 * 1970 *
GCAGC GCTGC CTGTT CGCGC C ATG GGG GCA CCG TGG GGC TCG CCG ACC GCG GCG
Met Gly Ala Pro Trp Gly Ser Pro Thr Ala Ala

1980 * 1990 * 2000 * 2010 * 2020 *
GCG GGC GGG CCG CGC GGC TGG CGC CGA GGC GCG GGG CTG CCA TGG ACC GTC TGT
Ala Gly Gly Arg Arg Gly Trp Arg Arg Gly Arg Gly Leu Pro Trp Thr Val Cys

2030 * 2040 * 2050 * 2060 * 2070 * 2080 *
GTG CTG GCG GCC GGC GGC TTG ACG TGT ACG GCG CTG ATC ACC TAC GCT TGC TGG
Val Leu Ala Ala Ala Gly Leu Thr Cys Thr Ala Leu Ile Thr Tyr Ala Cys Trp

2090 * 2100 * 2110 * 2120 * 2130 *
GGG CAG CTG CCG CCG CTG CCC TGG GCG TCG CCA ACC CCG TCG CGA CCG GTG GGC
Gly Gln Leu Pro Pro Leu Trp Ala Ser Pro Thr Pro Ser Arg Pro Val Gly

2140 * 2150 * 2160 * 2170 * 2180 * 2190 *
CTG CTG CTG TGG TGG GAG GAG CCC TTC GGG GGC CGC GAT AGC GCC CCG AGG CCG CCC
Val Leu Leu Trp Trp Glu Pro Phe Gly Gly Arg Asp Ser Ala Pro Arg Pro Pro

2200 * 2210 * 2220 * 2230 * 2240 *
CCT GAC TGC CCG CTG CGC TTC AAC ATC AGC GGC TGC CGC CTG CTC ACC GAC CGC
Pro Asp Cys Pro Leu Arg Phe Asn Ile Ser Gly Cys Arg Leu Leu Thr Asp Arg

2250 * 2260 * 2270 * 2280 * 2290 *
GCG TCC TAC GGA GAG GCT CAG GCC GTG CTT TTC CAC CAC CGC GAC CTC GTG AAG
Ala Ser Tyr Gly Glu Ala Ala Val Leu Phe His His Arg Asp Leu Val Lys

FIG. 4E

FOOTNOTES SHEET

FIG. 4F

2300 *	2310 *	2320 *	2330 *	2340 *	2350 *
GGG CCC CCC GAC TGG CCC CCG CCC TGG GGC ATC CAG GCG CAC ACT GCC GAG GAG					
Gly Pro Pro Asp Trp Trp Pro Pro Trp Gly Ile Gln Ala His Thr Ala Glu Glu					
2360 *	2370 *	2380 *	2390 *	2400 *	
GTG GAT CTG CGC GTG TTG GAC TAC GAG GAG GCA GCG GCG GCA GAA GCC CTG					
Val Asp Leu Arg Val Leu Asp Tyr Glu Glu Ala Ala Ala Glu Ala Leu					
2410 *	2420 *	2430 *	2440 *	2450 *	2460 *
GCG ACC TCC AGC CCC AGG CCC CCG GGC CAG CGC TGG GTT TGG ATG AAC TTC GAG					
Ala Thr Ser Ser Pro Arg Pro Pro Gly Gln Arg Trp Val Trp Met Asn Phe Gln					
2470 *	2480 *	2490 *	2500 *	2510 *	
TCG CCC TCG CAC TCC CCG GGC CTG CGA AGC CTG GCA AGT AAC CTC TTC AAC TGG					
Ser Pro Ser His ser Pro Gly Leu Arg Ser Leu Ala Ser Asn Leu Phe Asn Trp					
2520 *	2530 *	2540 *	2550 *	2560 *	
ACG CTC TCC TAC CCG GCG GAC TCG GAC GTC TTT GTG CCT TAT GGC TAC CTC TAC					
Thr Leu Ser Tyr Arg Ala Asp Ser Asp Val Phe Val Pro Tyr Gly Tyr Leu Tyr					
2570 *	2580 *	2590 *	2600 *	2610 *	2620 *
CCC AGA AGC CAC CCC GGC GAC CCC TCA GGC CTG GCC CCG CCA CTG TCC AGG					
Pro Arg Ser His Pro Gly Asp Pro Pro Ser Gly Leu Ala Pro Pro Leu Ser Arg					
2630 *	2640 *	2650 *	2660 *	2670 *	
AAA CAG GGC CTG GTG GCA TGG GTG GTG AGC CAC TGG GAC GAG CGC CAG GCC CGG					
Lys Gln Gly Leu Val Ala Trp Val Val Ser His Trp Asp Glu Arg Gln Ala Arg					

2680	2690	2700	2710	2720	2730
* GTC CGC TAC TAC CAC CAA CAT GTG ACC GTG GAC GTG TTC GGC CGG	* Val Arg Tyr Tyr His Gln Leu Ser Gln His Val Thr Val Asp Val Phe Gly Arg				
2740	2750	2760	2770	2780	
* CGC GGC CCC GGG CAG CCG GTG CCC GAA ATT GGG CTC CTG CAC ACA GTG GCC CGC	* Gly Gly Pro Gly Gln Pro Val Pro Gln Ile Gly Leu Leu His Thr Val Ala Arg				
2790	2800	2810	2820	2830	
* TAC AAG TTC TAC TAC GCT TTC GAG AAC TCG CAG CAC CTG GAT TAT ATC ACC GAG	* Tyr Lys Phe Tyr Leu Ala Phe Gln Asn Ser Gln His Leu Asp Tyr Ile Thr Glu				
2840	2850	2860	2870	2880	2890
* AAG CTC TGG CGC AAC GCG TTG CTC GCT GGG GCG GTG CCG GTG GTG CTG GGC CCA	* Lys Leu Trp Arg Asn Ala Leu Leu Ala Gly Ala Val Pro Val Val Leu Gly Pro				
2900	2910	2920	2930	2940	
* GAC CGT GCC AAC TAC GAG CCG TTT GTG CCC CGC GGC GCC TTC ATC CAC GTG GAC	* Asp Arg Ala Asn Tyr Glu Arg Phe Val Pro Arg Gly Ala Phe Ile His Val Asp				
2950	2960	2970	2980	2990	3000
* GAC TTC CCA AGT GCC TCC TCC TCC TCG TAC CTG CTT TTC CTC GAC CGC AAC	* Asp Phe Pro Ser Ala Ser Ser Ser Leu Ala Ser Tyr Tyr Leu Phe Leu Asp Arg Asn				
3010	3020	3030	3040	3050	
* CCC GCG GTC TAT CGC CGC TAC TTC CAC TGG CGC CGG AGC TAC GCT GTC CAC ATC	* Pro Ala Val Tyr Arg Arg Tyr Phe His Trp Arg Arg Ser Tyr Ala Val His Ile				

FIG. 46

3060	3070	3080	3090	3100
* ACC TCC TTC TGG GAC GAG CCT TGG TGC CGG GTG TGC CAG GCT GTA CAG AGG GCT				*
Thr Ser Phe Trp Asp Glu Pro Trp Cys Arg Val Cys Gln Ala Val Gln Arg Ala				
3110	3120	3130	3140	3150
* GGG GAC CGG CCC AAG AGC ATA CGG AAC TTG GCC AGC TGG TTC GAG CGG TGA A		*	*	*
Gly Asp Arg Pro Lys Ser Ile Arg Asn Leu Ala Ser Trp Phe Glu Arg ***				
3170	3180	3190	3200	3210
* GCCGC GCTCC CCTGG AAGCG ACCCA GGGGA GGGCA AGTTG TCAGC TTTT GATCC TCTAC		*	*	*
3230	3240	3250	3260	3270
* TGTGC ATCTC CTTGA CGGCC GCATC ATGGG AGTAA GTTCT TCAAA CACCC ATTTT TGCTC		*	*	*
3290	3300	3310	3320	3330
* TATGG GAAAA AAACG ATTTA CCAAT TAATA TTACT CAGCA CAGAG ATGGG GGCCC GGTTT		*	*	*
3350	3360	3370	3380	3390
* CCATA TTTT TGCAC AGCTA GCAAT TGGGC TCCCT TTGCT GCTGA TGGGC ATCAT TGTTT		*	*	*
3410	3420	3430	3440	3450
* AGGGG TGAAG GAGGG GTTTC TTCCT CACCT TGTA CCAGT GCAGA AATGA AATAG CTTAG		*	*	*
3470	3480	3490	3500	3510
* CGGCA AGAAG CCGTT GAGGC GGTTT CCTGA ATTTC CCCAT CTGCC ACAGG CCATA TTTGT		*	*	*

FIG. 4H

3530 * 3540 * 3550 * 3560 * 3570 * 3580 *
GGCCC GTGCA GCTTC CAAAT CTCAT ACACA ACTGT TCCCG ATTCA CGTTT TTCTG GACCA
3590 * 3600 * 3610 * 3620 * 3630 * 3640 *
AGGTG AAGCA AATTT GTGGT TGTAG AAGGA GCCTT GTTGG TGGAG AGTGG AAGGA CTGTG
GCTGC AG

FIG. 4I

DOCKET SHEET

pFT-3 DNA	ATGGGGGCACCGTGGGGCTCGCCGACGGCGGGCGGGCGGGCGGGCGGGT	
pFT-3 AA	1 M G A P W G S P T A A A G G R R G W18	
Lewis AA	1 M D . P L G A A K P Q W P W13	
pFT-3 DNA	GGCGGAGGCGGGGGCTGCCATGGACCGTCTGTGTGGCGGCC-----	
pFT-3 AA	19 R R G R G L P W T V C V L A A . . 33	
Lewis AA	14 R R C . L A A L L 22	
pFT-3 DNA	--GCCCGGCTTGACGTGTACGGCGGATCACCTAC-----GCT	
pFT-3 AA	34. A G L T C T A L I T Y . . A 45	
Lewis AA	23F Q L L V A V C F F S Y L R V 36	
pFT-3 DNA	TGCTGGGGGCAGCTGCCCGCGCTGCCCTGGGCG-----TCGCCA-----	
pFT-3 AA	46 C W G Q L P P P L P W A . . . S P . 58	
Lewis AA	37 S R D D A T G S P R A P S G S S R Q54	
pFT-3 DNA	-----ACCCCGTCGCGACCG---GTGGGCGTGTGTGTGG---TGGGAGC	
pFT-3 AA	59 . . T P S R P . V G V L L W . W E 71	
Lewis AA	55 D T T P T R P T L L I L L W T W . 70	
pFT-3 DNA	CCTTCGGGGCGCGATAGCGCCCGAGGCGGCCCTGACTGC	
pFT-3 AA	72P F G G R D S A P R P P P D C 86	
Lewis AA	71P F H I P V A L S R C . . S 82	

FIG.5A

pFT-3 DNA	CCGCTGCGCTTCAACATCAGCGGCTGCCGCTGCTCACCACCGCGCGCTCCTA	
pFT-3 AA	87 P L R F N I S G C R L L T D R A S Y104	
Lewis AA	83 E M V P G T A D C H I T A D R K V Y100	
pFT-3 DNA	CGGAGAGGCTCAGCGCGTGTCTTTCCACCACCGCGACCTCGTGAAGGGCCCC	
pFT-3 AA	105 G E A Q A V L F H H R D L V K G P 121	
Lewis AA	101 P Q A D T V I V H H W D I M S N P 117	
pFT-3 DNA	CCGACTGGCCCCCGCCCTGGGGCATCCAGGCGCACACTGCCGAG	
pFT-3 AA	122P D W P P P W G I Q A H T A E 136	
Lewis AA	118K S R L P P 123	
pFT-3 DNA	GAGGTGGATCTGCGCGTGTGGACTACGAGGAGCGCGCGCGGCGAGAAGC	
pFT-3 AA	137 E V D L R V L D Y E E A A A A E A154	
Lewis AA	124 124	
pFT-3 DNA	CCTGGCGACCTCCAGCCCCAGGCCCGCGCGCGCTGGGTTGGATGAACT	
pFT-3 AA	155 L A T S S P R P P P G Q R W V W M N 171	
Lewis AA	124 136	
pFT-3 DNA	TCGAGTCGCCCTCGCACTCCCCGGGGCTGCGAAGCCTGGCAAGT	
pFT-3 AA	172F E S P S H S P G L R S L A S 186	
Lewis AA	137L E P P P N C Q H L E A L D . 150	

FIG.5B

pFT-3 DNA	AACCTCTTCAACTGGACGCTCTCTACCGGGGAGCTCGGACGTCTTTGTGCC	
pFT-3 AA	187 N L F N W T L S Y R A D S D V F V P204	
Lewis AA	151 R Y F N L T M S Y R S D S D I F T P168	
pFT-3 DNA	TTATGGCTACCTCTACCCAGAAGC---CACCCCGGACCCCGCCCTCAGGCC	
pFT-3 AA	205 Y G Y L Y P R S . H P G D P P S G 220	
Lewis AA	169 Y G W L E P W S G Q P A H P P . 183	
pFT-3 DNA	TGGCCCCGCCACTGTCCAGAAACAGGGGCTGGTGGCATGGGTG	
pFT-3 AA	221L A P P L S R K Q G L V A W V 235	
Lewis AA	184L N . L S A K T E L V A W A 196	
pFT-3 DNA	GTGAGCCACTGGGACGAGCGCCAGGCCGGGTCCGCTACTACCACCACTGAG	
pFT-3 AA	236 V S H W D E R Q A R V R Y Y H Q L S253	
Lewis AA	197 V S N W K P D S A R V R Y Y Q S L Q214	
pFT-3 DNA	CCAACATGTGACCGTGGACGTGTTCCGGCCGGGCGGCGGCGAGCCGGTGC	
pFT-3 AA	254 Q H V T V D V F G R G G P G Q P V 270	
Lewis AA	215 A H L K V D V Y G R S . H K P L 229	
pFT-3 DNA	CCGAAATTGGGCTCTGCACACAGTGGCCCGCTACAAGTTCTAC	
pFT-3 AA	271P E I G L L H T V A R Y K F Y 285	
Lewis AA	230P K G T M M E T L S R Y K F Y 244	

FIG. 5C

pFT-3 DNA	CTGGCTTTCGAGAACTCGCAGCACCTGGATTATATACCGAGAAAGCTCTGGCG	
pFT-3 AA	286 L A F E N S Q H L D Y I T E K L W R303	
Lewis AA	245 L A F E N S L H P D Y I T E K L W R262	
pFT-3 DNA	CAACGCGTTGCTCGTGGGGCGGTGCCGTGTGTGGGCCCGACCGTGCCCA	
pFT-3 AA	304 N A L L A G A V P V V L G P D R A 320	
Lewis AA	263 N A L E A W A V V L G P S R S 279	
pFT-3 DNA	ACTACGAGCGCTTGTGCCCGCGCGCCTTCATCCACGTGGAC	
pFT-3 AA	321N Y E R F V P R G A F I H V D 335	
Lewis AA	280N Y E R F L P P D A F I H V D 294	
pFT-3 DNA	GACTTCCCAAGTGCCTCCTCCCTGGCCTCGTACCTGCTTTTCCTCGACCGCAA	
pFT-3 AA	336 D F P S A S S L A S Y L L F L D R N353	
Lewis AA	295 D F Q S P K D L A R Y L Q E L D K D312	
pFT-3 DNA	CCCCGGGTCTATCGCCGCTACTTCCACTGGCGC-----CGGA	
pFT-3 AA	354 P A V Y R R Y F H W R . . . R 365	
Lewis AA	313 H A R Y L S Y F R W R E T L R P R 329	
pFT-3 DNA	GCTACGCTGTCCACATCACCTCCTTC---TGGGACGAGCCTTGG	
pFT-3 AA	366S Y A V H I T S F . W D E P W 379	
Lewis AA	330S F S W A L D . . F 337	

FIG.5D

pFT-3 DNA	TGCCGGGTGTGCCAGGCTGTACAGAGGGCTGGGGACCGGCCCAAGAGCATACG	
pFT-3 AA	380 C R V C Q A V Q R A G D R P K S I R397	
Lewis AA	338 C K A C W K L Q Q E S . R Y Q T V R354	
pFT-3 DNA	GAACTTGGCCAGCTGGTTCGAGCGGTGA	
pFT-3 AA	398 N L A S W F E R 405	
Lewis AA	355 S I A A W F T . 361	

FIG. 5E

...-120 TTTATGACAAGCTGTGTCTATAAATTATAACAGCTTCTCTCAGGACACTGTGGCCAGGAAG

-60 TGGGTGATCTTCCCTTAATGACCCCTCACTCCCTCTCTCCCTCTCTCCAGCTACTCTGACCC

1 M D P L G P A K P Q W L W R R C L A G L
ATGGATCCCCTGGCCAGCCAGCCACAGTGGCTGTGGCGCGCTGTCTGGCCGGGCTG
ATGGATCCCCTGGTGAGCCAGCCACAATGGCCATGGCGCGCTGTCTGGCGGCACTG A
P

61
L F Q L L V A V C F F S Y L R V S R D D
 CTGTTTCAGCTGCTGGTGGCTGTGTGTTTCTCTACCTGCGTGTGTCCGAGACGAT
 CTATTTACAGCTGCTGGTGGCTGTGTGTTTCTCTACCTGCGTGTGTCCGAGACGAT

121 A T G S P R P G L M A V E P V T G A P N
GCCACTGGATCCCCCTAGGCCAGGCTTATGGCAGTGGAACTGTACCGGGCTCCCAAT
GCCACTGGATCCCCCTAGG-----GCTCCAGT S

181 G S R C Q D S M A T P A H P T L L I L L
GGTCCCGCTGCCAGGACAGCATGGCGACCCCTGCGCCACCCCTACTGATCCTGCTG
GGTCCCTCCGACAGGACAC-----ACTCCACCCGCCCCACCCCTCCTGATCCTGCTA
S R S R T R

FIG. 6A

W T W P F N T P V A L P R C S E M V P G
241 TGGACGTGGCCCTTTAAACACACCCGTGGCTCTGCCCGCTGCTCAGAGATGGTCCCGGC
TGGACATGGCCCTTCCACATCCCTGTGGCTCTGTCCCGCTGTTTCAGAGATGGTCCCGGC

A A D C N I T A D S S V Y P Q A D A V I
301 GGGCCGACTGCAACATCACTGCCGACTCCAGTGTTGTTACCCACAGGACGCGGTTCATC
ACAGCCGACTGCCACATCACTGCCGACTCCAGTGAAGTGTACCCACAGGACGCGGTTCATC

V H H W D I M Y N P S A N L P P P T R P
361 GTGCACCACTGGGATATCATGTCAACCCCAAGTGCACGCTCCACCTTCCCGAGGCCG
GTGCACCACTGGGATATCATGTCAACCCCAAGTGCACGCTCCACCTTCCCGAGGCCG

Q G Q R W I W F S M E S P S N C R H L E
421 CAGGGCAGCGCTGGATCTGGTTTCAGCATGGAGTCCCCCAGCAACTGCCGACCTGGAA
CAGGGCAGCGCTGGATCTGGTTCAACTTGGAGCCACCCCTAACTGCCAGCACCTGGAA

A L D G Y F N L T M S Y R S D S D I F T
481 GCCCTGGACGGATACTTCAATCTCACCATGTCTACCGCAGCGACTCCGACATCTTCACG
GCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGCGACTCCGACATCTTCACG

P Y G W L E P W S G Q P A H P P L N L S
541 CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG
CCCTACGGCTGGAGCCGTGGTCCGGCCAGCCTGCCACCCACCGCTCAACCTCTCG

FIG. 6B

601 A K T E L V A W A V S N W K P D S A R V
GCCAAGACOGAGCTGGTGGCCCTGGCGGTCCAACTGGAAGCCGGACTCGGCCAGGGTG
GCCAAGACOGAGCTGGTGGCCCTGGCGGTCCAACTGGAAGCCGGACTCGGCCAGGGTG

661 R Y Y Q S L Q A H L K V D V Y G R S H K
CGTACTACCAGAGCCTGCAGGCTCATCTCAAGTGGACGTGTACGGACGCTCCACAAG
CGTACTACCAGAGCCTGCAGGCTCATCTCAAGTGGACGTGTACGGACGCTCCACAAG

721 P L P K G T M M E T L S R Y K F Y L A F
CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGGTACAAGTTCTATCTGGCCCTTC
CCCCTGCCCAAGGGACCATGATGGAGACGCTGTCCCGGTACAAGTTCTATCTGGCCCTTC

781 E N S L H P D Y I T E K L W R N A L E A
GAGAACTCCTTGACCCCGACTACATCACCAGAGAAGCTGTGGAGGAACGCCCTGGAGGCC
GAGAACTCCTTGACCCCGACTACATCACCAGAGAAGCTGTGGAGGAACGCCCTGGAGGCC

841 W A V P V V L G P S R S N Y E R F L P P
TGGCCGTGCCCGTGGTGTGGTGGCCCGCCAGCAGAACCACTACGAGAGGTTCTTCCGCCCC
TGGCCGTGCCCGTGGTGTGGTGGCCCGCCAGCAGAACCACTACGAGAGGTTCTTCCGCCCC

901 D A F I H V D D F Q S P K D L A R Y L Q
GAGCCTTCATCCACGTGGATGACTTCCAGAGCCCCAAGGACCTGGCCCGGTACCTGCAG
GAGCCTTCATCCACGTGGACGACTTCCAGAGCCCCAAGGACCTGGCCCGGTACCTGCAG

961 E L D K D H A R Y L S Y F R W R E T L R
GAGCTGGACAAGGACCAAGCCCGTACCTGAGTACTTTCGCTGGCGGAGACGCTGCGG
GAGCTGGACAAGGACCAAGCCCGTACCTGAGTACTTTCGCTGGCGGAGACGCTGCGG

FIG. 6C

P R S F S W A L A F C K A C W K L Q Q E
1021 CCTCGCTCCTTCAGCTGGGCACTGGCTTTCTGCAAGGCCTGCTGGAAGCTGCAGCAGGAA
CCTCGCTCCTTCAGCTGGGCACTGGATTTCTGCAAGGCCTGCTGGAAGCTGCAGCAGGAA
D

S R Y Q T V R S I A A W F T U
1081 TCCAGGTACACAGACGGTGCGCAGCATAGCGGCTTGGTTACCTGAGAGGCCGCGCATGGGG
TCCAGGTACACAGACGGTGCGCAGCATAGCGGCTTGGTTACCTGA

1141 CCTGGGCTGCCAGGGACCTCACTTCCAGGGCCTCACCTACCTAGGTC // TCTAGA

FIG. 6D

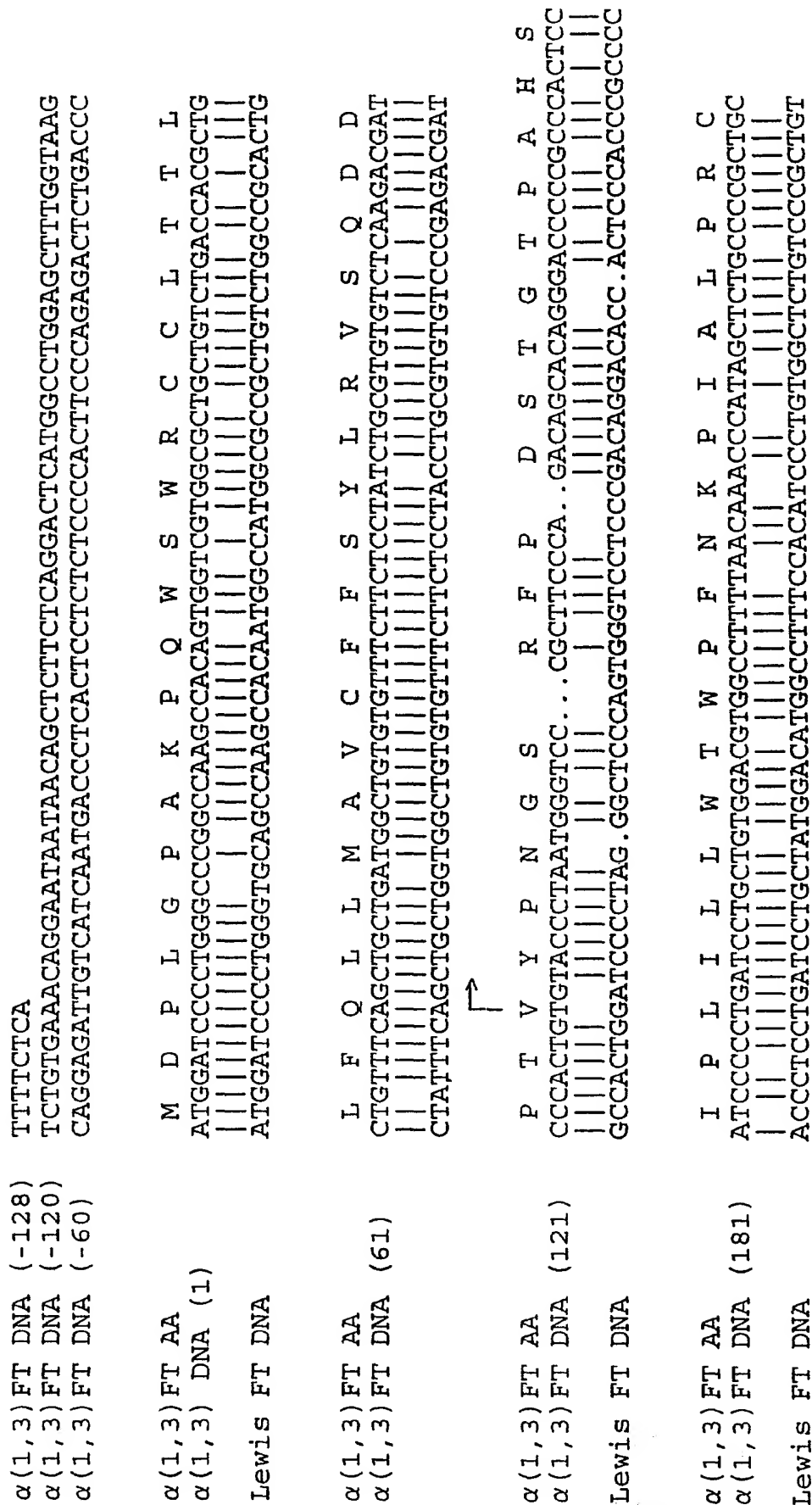


FIG. 7A

S E M V P G T A D C N I T A D R K V Y P
TCAGAGATGGTGCCTGGCACGGCTGACTGCAACATCACTGCCGACCGCAAGGTGTATCCA
|||||
TCAGAGATGGTGCCTGGCACAGCCGACTGCCACATCACTGCCGACCGCAAGGTGTATACCCA

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (241)
Lewis FT DNA

Q A D A V I V H H R E V M Y N P S A Q L
CAGGCAGACGGGTTCATCGTGCAACCCAGAGGTCATGTACAACCCAGTGCCAGCTC
|||||
CAGGCAGACACGGTTCATCGTGCAACCCAGTGGATATCATGTCCAACCCTAAGTCACGCCTC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (301)
Lewis FT DNA

P R S P R R Q G Q R W I W F S M E S P S
CCACGCTCCCCGAGGCGGCGAGCGGATGGATCTGGTTCAAGCATGGAGTCCCCAAGC
|||||
CCACCTTCCCCGAGGCGGCGAGGCGGCTGGATCTGGTTCAACTTGGAGCCACCCCT

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (361)
Lewis FT DNA

H C W Q L K A M D G Y F N L T M S Y R S
CACTGCTGGCAGCTGAAGCCATGGACGGATACTTCAATCTCACCATGTCTACCGCAGC
|||||
AACTGCCAGCACCTGGAAGCCCTGGACAGATACTTCAATCTCACCATGTCTACCGCAGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (421)
Lewis FT DNA

D S D I F T P Y G W L E P W S G Q P A H
GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC
|||||
GACTCCGACATCTTCACGCCCTACGGCTGGCTGGAGCCGTGGTCCGGCCAGCCTGCCAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (481)
Lewis FT DNA

FIG. 7B

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (541)
Lewis FT DNA

P P L N L S A K T E L V A W A V S N W G
CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGCAGTGTCCAACTGGGGG
|||||
CCACCGCTCAACCTCTCGGCCAAGACCGAGCTGGTGGCCTGGGCGGTGTCCAACTGGAAG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (601)
Lewis FT DNA

P N S A R V R Y Y Q S L Q A H L K V D V
CCAAACTCCGCCAGGTGGTGGTACTACTACAGAGCCTGCAGGCCCATCTCAAGGTGGACGTG
|||||
CCGGACTCAGCCAGGTGGTGGTACTACTACAGAGCCTGCAGGCTCATCTCAAGGTGGACGTG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (661)
Lewis FT DNA

Y G R S H K P L P Q G T M E T L S R Y
TACGGACGCTCCACAAAGCCCTGCCCCAGGAACCATGATGGAGACGCTGTCCCGGTAC
|||||
TACGGACGCTCCACAAAGCCCTGCCCCAAGGGACCATGATGGAGACGCTGTCCCGGTAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (721)
Lewis FT DNA

K F Y L A F E N S L H P D Y I T E K L W
AAGTTCTATCTGGCCTTCGAGAACTCCTTGCACCCCGACTACATCACCGAGAAGCTGTGG
|||||
AAGTTCTACCTGGCCTTCGAGAACTCCTTGCACCCCGACTACATCACCGAGAAGCTGTGG

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (781)
Lewis FT DNA

R N A L E A W A V P V V L G P S R S N Y
AGGAACGCCCTGGAGGCCTGGGCCGTGGCCCGTGGTGGTGGCCCGCAGCAGAACTACTAC
|||||
AGGAACGCCCTGGAGGCCTGGGCCGTGGCCCGTGGTGGTGGCCCGCAGCAGAACTACTAC

FIG. 7C

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (841)
Lewis FT DNA

E R F L P P D A F I H V D D F Q S P K D
GAGAGTTCTCCACCCGACGCTTCCATCCACGTGGACGACTTCCAGAGCCCCAAGGAC
|||||
GAGAGTTCTCCACCCGACGCTTCCATCCACGTGGACGACTTCCAGAGCCCCAAGGAC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (901)
Lewis FT DNA

L A R Y L Q E L D K D H A R Y L S Y F R
CTGGCCCGGTACTGACGAGCTGGACAGGACCAAGGACCCCGCTACCTGAGCTACTTTCGC
|||||
CTGGCCCGGTACTGACGAGCTGGACAGGACCAAGGACCCCGCTACCTGAGCTACTTTCGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (961)
Lewis FT DNA

W R E T L R P R S F S W A L A F C K A C
TGGCGGAGACGCTGGCGCCTCGCTCCTTCAGCTGGGCACTCGCTTCTGCAAGGCCTGC
|||||
TGGCGGAGACGCTGGCGCCTCGCTCCTTCAGCTGGGCACTCGATTTCTGCAAGGCCTGC

$\alpha(1,3)$ FT AA
 $\alpha(1,3)$ FT DNA (1021)
Lewis FT DNA

W K L Q E E S R Y Q T R G I A A W F T Stop
TGGAAACTGCAGGAGGAATCCAGGTACCAGACACGCGGC...ATAGCGGCTTGGTTACCTGA
|||||
TGGAAACTGCAGGAGGAATCCAGGTACCAGACGCTGGCGAGCATAGCGGCTTGGTTACCTGA

GAGGCTGGTGGGGCCTGGGCTGCCAGGAACCTCATTTCTGGGGCCTCACCTGAGTG
GGGCGCTCATCTAAGGACTCGTTTGCTGAAGCTTCACTGCTGAGGACTCACCT
GCTGGGACGGTCACTGTGACGCTTCACTGCTGGGATTCACCTGAGGATTCCTGCTG
ACTTCTGGGGCCTCACCTGCTGGAGTCTTGGTGGCCAGGATGCTTACCTGGGA
TTTCACTGCTGGCTTCCAGGAGCGTCCCTGCGGAAGCCTGGCTGCTGGGATGCTC
CTGGGACTTTGCTACTGGGACCTCGGCTGTTGGGACCTTACCTGCTGGGACCTGCT
CCCAGAGACCTTCCACACTGAATCTACCTGCTAGGAGCCTCACCTGCTGGGACCTCAC
CCTGGAGGCACTGGGGCCTGGGAAC

FIG. 7D

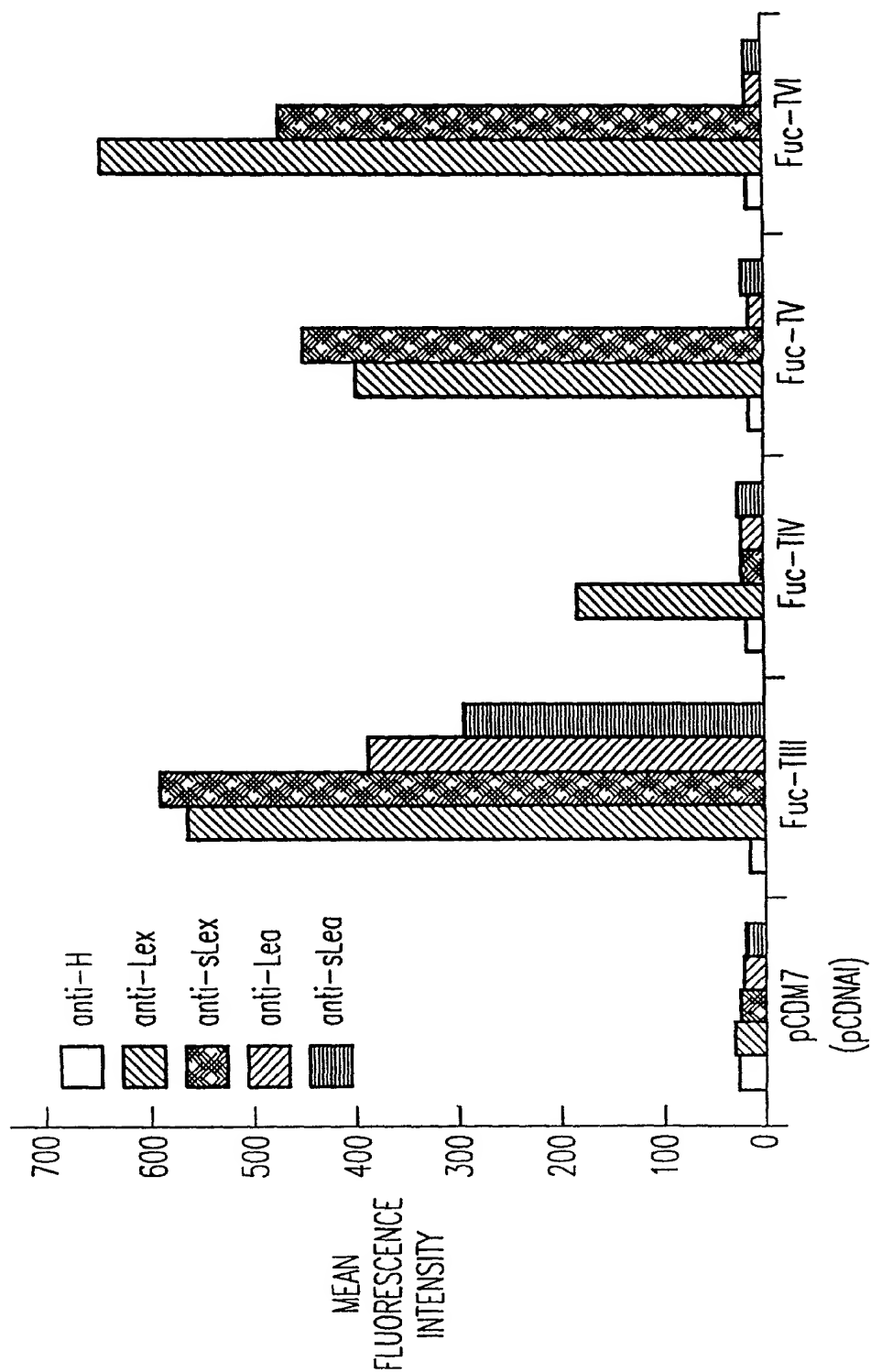


FIG. 8

FIG. 8